

Time efficient parallel imaging for 2D multi-slice MRI with continuously moving table

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Introduction

In whole body MRI with continuously moving table (CMT-MRI) the acquisition time is an important issue. In particular for examinations performed during breath holding, the number of required breath holding phases should be small and the duration of each breath holding phase as short as possible. In the 2D multi-slice approach to CMT-MRI investigated here, parallel imaging with no higher reduction factors than $R = 2$ is feasible to speedup the acquisition due to the used coils and the acquisition scheme. In this study the recently introduced z-GRAPPA method [1] is applied to accelerate CMT-MRI. In contrast to the conventional GRAPPA algorithm [2], this method avoids the acquisition of additional data for calibration, but combines k-space lines from adjacent slices for coil weight computation. For a clinically relevant protocol, the duration of one breath holding phase could be reduced by 18 %.

Methods

Fig. 1 depicts the principle of the z-GRAPPA method. For all slices k-spaces are undersampled by a factor of R and for adjacent slices the acquired lines are shifted by one line (Fig. 1, step a). No additional calibration lines are required, but calibration data is obtained by combining k-space lines from adjacent slices (Fig. 1, step b). The coil weights computed from that data are used to reconstruct the missing k-space lines (Fig. 1, step c).

Data was acquired from one healthy volunteer using a FLASH sequence with continuously moving table on a 1.5T scanner (Magnetom Avanto, Siemens Erlangen, Germany). The sliding multi slice (SMS) technique [3] was used for all measurements, which acquires each k-space along the same trajectory within the magnet, thus avoiding distortions due to gradient non-linearities. A fully sampled acquisition, conventional GRAPPA acquisitions with $R = 2$ and $R = 3$ and a z-GRAPPA acquisition with $R = 2$ were performed. For the conventional GRAPPA acquisitions 12 ($R = 2$) respectively 17 ($R = 3$) additional k-space lines were acquired to have 26 lines available for calibration in each case. The additionally acquired lines were also used for the image reconstruction. The characteristic parameters of all acquisitions are summarized in table 1. The identical acquisition times for z-GRAPPA with $R = 2$ and conventional GRAPPA with $R = 3$ despite different effective accelerations are due to the different number of dummy scans required to apply the SMS reordering scheme. Further sequence parameters which all acquisitions had in common were: TR/TE = 111ms/2.03ms, 17 slices, slice thickness = 5mm, slice gap = 0.85mm, in-plane resolution = $1.6 \times 1.2 \text{ mm}^2$, field-of-view = $304 \times 380 \text{ mm}^2$, partial Fourier factor = $7/8$.

The signal-to-noise ratio (SNR) was computed for each slice of the different data sets in a region of interest (ROI) in the lower spinal muscles (see upper left image in Fig. 2 for an example). A difference method [4] was used to assess the SNR, which estimates the signal from the mean image of two identical acquisitions and the noise from their difference image. Hence, all acquisitions were performed twice. For each pair of acquisitions it was verified by visual inspection that interscan motion was negligible for each ROI.

For large slice gaps the z-GRAPPA method potentially yields inconsistent calibration data. To assess this limitation, the fully sampled data was retrospectively undersampled and only every second slice (effective slice gap = 6.7mm) or third slice (effective slice gap = 12.55mm), respectively, was used for z-GRAPPA based calibration.

Results

Fig. 2 shows images reconstructed from the different acquisitions (first two lines) and from the retrospectively undersampled data with different slice gaps (last line). The anatomic differences between the images in the area of the liver are due to different breath holding positions in the different acquisitions. Hardly any differences of the signal quality are visible between the reconstruction from the fully sampled data and the GRAPPA reconstruction with $R = 2$. In the z-GRAPPA reconstruction with $R = 2$ the noise is slightly increased, but no ghosting artifacts are visible. The conventional GRAPPA reconstruction with $R = 3$ shows clearly visible artifacts in the area of the liver (indicated by the white arrow in Fig. 2). The z-GRAPPA reconstruction with a gap of 6.7mm shows no visible artifacts, while clear ghosting artifacts appear in the z-GRAPPA reconstruction with a gap of 12.55mm. The SNR over all slices of the data sets described in table 1 is shown in Fig. 3. The SNR values measured for the fully sampled data are clearly highest. For the GRAPPA based reconstructions the SNR values are lower and relatively close together for most slices. In all cases the SNR measured for conventional GRAPPA with $R = 2$ (which uses the additional calibration data for the reconstruction) is above the SNR measured for z-GRAPPA with $R = 2$, and the latter is above the SNR for conventional GRAPPA with $R = 3$.

Discussion

The z-GRAPPA method was successfully applied to CMT-MRI to reduce the acquisition time for a clinically relevant protocol by 18% compared to conventional GRAPPA with the same reduction factor. One breath holding phase can thus be shortened from 22 seconds to 18 seconds. Thus z-GRAPPA provides a means of accelerating 2D multi-slice CMT-MRI slightly beyond the limits of conventional parallel imaging. To obtain consistent coil weights the z-GRAPPA method requires that both the image content and the coil sensitivities change slowly in slice direction. Hence, the slice gap and the slice thickness are its main limitations. The obtained results and the findings in [1] show however, that the method collapses only for uncommonly large slice gaps.

In future work the applicability of z-GRAPPA in conjunction with CMT-MRI has to be evaluated clinically. It has to be examined whether the achievable SNR is sufficient for diagnosis and protocols have to be established which allow the reconstruction of artifact free images regardless of the imaged anatomy.

References

[1] M. Honal, et al.: Magn Reson Med, in press, 2008. [2] M. Griswold, et al.: Magn Reson Med, 2002. 47(6): p. 1202-1210. [3] H. P. Fautz, et al.: Magn Reson Med, 2006. 55(2): p. 363-370. [4] O. Dietrich, et al.: J. Magn. Reson., 2007. 26: p. 375-385.

	Nb. of lines	Acq. time	Table speed	Eff. acceleration
Fully sampled	170	42s	5mm/s	1
GRAPPA $R = 2$	98	22s	10mm/s	1.73
GRAPPA $R = 3$	74	18s	12mm/s	2.29
z-GRAPPA $R = 2$	85	18s	12mm/s	2

Table 1: Acquisition parameters for the different data sets.

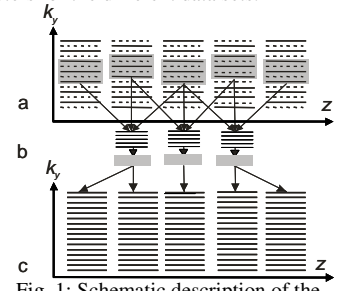


Fig. 1: Schematic description of the z-GRAPPA method.

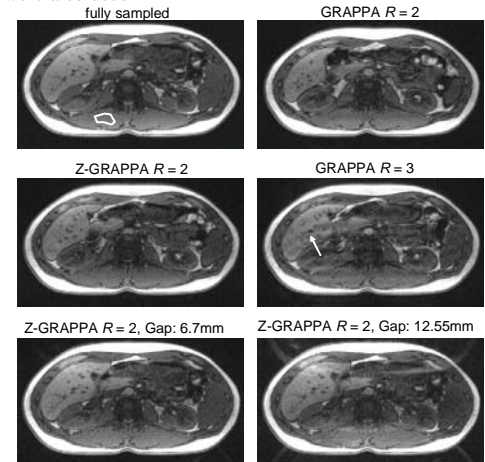


Fig. 2: Images of one slice position, reconstructed from the different data sets.

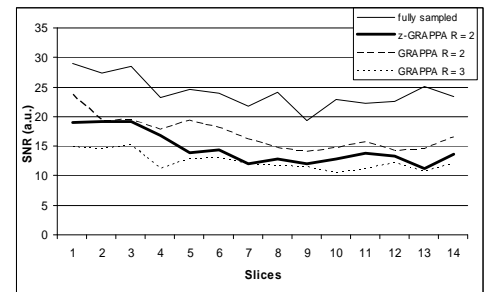


Fig. 3: SNR over all slices for the different acquisitions.